



AK

LOCUS AF134837 2982 bp DNA linear BCT 14-OCT-1999

DEFINITION Amycolatopsis mediterranei aspartokinase and aspartate-semialdehyde dehydrogenase operon, complete sequence.

ACCESSION AF134837

VERSION AF134837.1 GI:5733410

KEYWORDS

SOURCE Amycolatopsis mediterranei

ORGANISM Amycolatopsis mediterranei

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.

REFERENCE 1 (bases 1 to 2982)

AUTHORS Zhang,W., Jiang,W., Zhao,G., Yang,Y. and Chiao,J.

TITLE Sequence analysis and expression of the aspartokinase and aspartate semialdehyde dehydrogenase operon from rifamycin SV-producing amycolatopsis mediterranei

JOURNAL Gene 237 (2), 413-419 (1999)

PUBMED 10521665

REFERENCE 2 (bases 1 to 2982)

AUTHORS Zhang,W., Jiang,W.H., Zhao,G.P., Yang,Y.L. and Chiao,J.S.

TITLE Direct Submission

JOURNAL Submitted (13-MAR-1999) Microbiology. Shanghai Institute of Plant Physiology, Academia Sinica, 300 Fenglin Road, Shanghai, SH 200032, P.R.China

FEATURES Location/Qualifiers

source 1..2982
/organism="Amycolatopsis mediterranei"
/mol_type="genomic DNA"
/strain="U32"
/db_xref="taxon:33910"

gene 220..2525
/gene="aspartokinase and aspartate-semialdehyde dehydrogenase operon"

gene 220..1485

CDS 220..1485

/gene="askA"

/codon_start=1

/transl_table=11

/product="aspartokinase subunit A"

/protein_id="AAD49567.1"

/db_xref="GI:5733411"

/translation="MALVVQKYGGSSLESADRIK RVAERIVATKKAGNDVVVCSAMG
DTTDELLDLAQVNPAPPEREMDMLLTAGERISNSLVAMAIAAQGAEAWSFTGSQAGV
VTTSVHGNARIIDVTPSRVTEALDQGYIALVAGFQGV AQD TKDITTLGRGGS DTTAVA
LAAALNADVCEIYSDVDGVYTADPRVVPDAKKLDTVTYEEMLELAASGSKILHLSVE
YARRYGVPIRVRSYSDKPGTTVTGSIEEIPVEQALITGVAHDRSEAKITVTGVPDHT
GAAARIFRVIADAEIDIDMVLQNVSSSTVSGRTDITFTLSKANGAKAVKELEKVQAEIG
FESVLYDDHVGKVS VVGAGMRSHPGVTATFCEALAEAGVNIEINTSEIRISVLIRDA
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CDS 967..1485

/gene="askA"

/note="Orf2"

/codon_start=1

/transl_table=11

/product="aspartokinase subunit B"

/protein_id="AAD49568.1"

/db_xref="GI:5733412"

/translation="MEQALITGVAHDRSEAKITVTGVPDHTGAAARIFRVIADAEIDI
DMVLQNVSSSTVSGRTDITFTLSKANGAKAVKELEKVQAEIGFESVLYDDHVGKVS VVG
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DEEAVVYAGSGR"

CDS 1485..2525

/note="Orf3"

/codon_start=1

/transl_table=11

/product="aspartate semialdehyde dehydrogenase"

/protein_id="AAD49569.1"

/db_xref="GI:5733413"

/translation="MADGLRVGVVGATGQVGAVMRKLLAEREFP IAE LRYFASARSAG"

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 SGSGLAGVDELAGQVRAAAEHASLLTHDGAIDFPKPEKYVRPIAFNVLPMAGSIVDD
 GEFETDEEKKFRNESRKILSIPGLAVSCTCVRVPVFSGHSVSVNAEFERPLSVERATE
 LLTHAPGVELSEEPTPLQAAGNDPSYVGRIRVDPGVEGGRGLALFLSNDNLRKGAALN
 AIQIAELVAQQL"

ORIGIN

1 ggtaaccgcg tgtgtgtgc atcactcggg aggaagggtt ccgcgcattt cgttggtgtt
 61 gcggaagttt tacttcgcg acaccaccg gagggatccg cccacgtca agagggtggc
 121 gggccgcga agccccgta ggctcctgtt caaatcatgg gacggggggg ctctccgtg
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 421 atgtgtctca ccgcgggtga gcgcatctc aactcgtgg tcgcatggc gatcggggc
 481 caggcgcccg aggcgtggc gttaccggg tcgagggcg gcgtcgtac gacgtcgtg
 541 caggcaacg gcgcgtcat cgacgtcacg ccgagccggg tcaccgagcg gtcgaccag
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 661 acgtggggc gcggcggtc ggacaccacc gccgtcgcg tggccggcg gctgaacgc
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 1201 aagggtcagg cggagatcgg ctctgagtc gtctctacg acgaccagt cggcaagggtg
 1261 tcggtggtc gcgcgggat gcgtcgcac ccgggtgtca cggcgaggt ctgcgaagcg
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 1561 agcgggagt cccgatcgc gagctgcgt attcgttcg ggcgcgtcg gcggggtcga
 1621 aactccgtg gcgtgacac gaaatcaga tcgaggacg ctcgacggcg gatcgtccg
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 1861 tcgcgaatcc caactgcacc acgatcgccg cgatccgggt gctgaagccg ctgcacgacg
 1921 agggcggcct ggtccggtg gtgcgctga cgtaccaggc ggtgtccggc agcgggctgg
 1981 cggcgctga cgagctgcc gggcagggtc gggcgggcgc cgagcacgca tcgtctga
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 2101 tcaacgtct cccgatggcc gggtcattg tggacgacgg cgagttcgag acggacgaag
 2161 agaagaagtt ccgcaacgag agccgaaga tctgagcat cccgggtctc gccgtctcgt
 2221 gcacctcgt cgggtgccc gtgttctcg gccattcgt ctcggtgaac gcggagtctg
 2281 agcggccgt gtcggtcgag cgcgcgacgg agctgctgac ccacgcgcc ggcgtcgagc
 2341 tgtcggagga accgacacc ctgcaggcgg cgggcaacga ccgagctac gtcggccga
 2401 tccggtgga cccgggtgtc gaggcgggcc gcgggtcgc gctgttctc tcgaacgaca
 2461 acctgcgaa gggcgcgcg ctcaaccca tccagatcgc ggagctggtc gccagcagc
 2521 tctgacgacc acgcgaagg cccctaccg agcgcggtga gggccaacg cgtgaattca
 2581 cggccgggtt gcgcgtagc aggcgaggtg gcgcgtcttc aggaactcgc gttccggcgc
 2641 gccggttag gccagacga gcgcgtccg gtgcacgcc agcacctga actgctcgac
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 2761 gttccgggg tgggtccggc ctgcgcgtc cagccaaggc cggacgacgt ccagggcgag
 2821 cttggtcgg tcgtcttcc aggcgcgac gccctgtcc tcgcttctg gcgcggcgac
 2881 gagcgtagg cccgcagct tcgggcctt gtcagggtc tcgtcggcga acggaacat
 2941 ctgctcgtc gagccgaacc attggcgca ccagtactgc ag

//

[GENETYX : Amino Acid Sequence Homology Data]

Date : 2005.06.09

1st Amino Acid Sequence

File Name : Amycolatopsis mediterranei_askA.prj
Sequence Size : 421

2nd Amino Acid Sequence

File Name : M.methylotrophus ask.prj
Sequence Size : 409

Unit Size to Compare = 2

Pick up Location = 1

[49.633% / 409 aa] INT/OPT.Score : < 285/ 982 >

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1" MALIVQKYGG TSVANPERIR NVARRVARYK ALGHQVVVVV SAMSGETNRL ISLAKEIMQD PDPRELDVMV

71' TAGERISNSL VAMAIQAQA EAWSFTGSQA GVVTTSVHGN ARIIDVTPSR VTEALDQGYI ALVAGFQGVA
..*... ..*.. * ..*... ..*... ..*... ..*... ..*... ..*... ..*...
71" STGEQVTIGM TALALMELGI KAKSYTGTQV KILTDDAFTK ARILDIDEHN LKKDLDDGYV CVVAGFQGVV

141' QDTKDITTLG RGGSDTTAVA LAAALNADVC EIYSDVDGVY TADPRVVPDA KKLDTVTYEE MLELAASGSK
... ***** ***** ** *.. ***** *..***** *..***** *..***** ***** ***
141" ANG-NITTLG RGGSDTTGVA LAAALKADEC QIYTDVDGVY TTDPRVPEA RRLDKITFEE MLELASQGSK

211' ILHLRSVEYA RRYGVPIRVR SSYSK-PGT TVTGSIEEIP VEQALITGVA HDRSEAKITV TGVPDHTGAA
..*****. * * *.. ***** ** *.. *.. ***** *..***** ***** *
210" VLQIRSEFEA GKYKVKLRVL SSFEEEGDGT LITFEENEEN MEEPIISGIA FNRDEAKITV TGVPDKPGIA

280' ARIFRVIADA EIDIDMVLQN VSSTVSGRTD ITFTLSKANG AKAVKEL-EK VQAEIGFESV LYDDHVGKVS
..*..*** ..*... ** *.. ***** *.. ***** *.. ***** *..*****
280" YQILGPVADA NIDVDMIQN VGAD--GTTD FTFTVHKNEK NKALSILRDK VQGHQAREI SGDDKIAKVS

349' VVGAGMRSHP GVTATFCEAL AEAGVNIEII NTSEIRISVL IRDAQLDDAV RAIHEAFELG GDEEAVVYAG
***.***** *.. ..* ..*... ***** *.. ..* ..*... *****
348" VVGVMRSHV GIASQMFRITL AEEGINIQMI STSEIKIAVV IEEKYMEALV RVLHKAFFLE NA
```

AK-2

AL162756. Reports *Neisseria meningi...*[gi:7380091] Links

LOCUS NMA5Z2491 1218 bp DNA linear BCT 16-APR-2005

DEFINITION *Neisseria meningitidis* serogroup A strain Z2491 complete genome;
segment 5/7.

ACCESSION AL162756 REGION: complement(298368..299585)

VERSION AL162756.2 GI:7380091

KEYWORDS

SOURCE *Neisseria meningitidis* Z2491

ORGANISM *Neisseria meningitidis* Z2491

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; *Neisseria*.

REFERENCE 1 (bases 1 to 1218)

AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,

Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,

Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,

Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,

Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,

Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.

TITLE Complete DNA sequence of a serogroup A strain of *Neisseria*
meningitidis Z2491

JOURNAL Nature 404 (6777), 502-506 (2000)

PUBMED 10761919

REFERENCE 2 (bases 1 to 1218)

AUTHORS Parkhill,J.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the *Neisseria*
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

COMMENT Notes:

Details of *N. meningitidis* sequencing at the Sanger Centre are
available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).

FEATURES	Location/Qualifiers
source	1..1218 /organism="Neisseria meningitidis Z2491" /mol_type="genomic DNA" /strain="Z2491" /db_xref="taxon:122587" /note="serogroup: A"
gene	1..1218 /gene="lysC"
CDS	1..1218 /gene="lysC" /EC_number="2.7.2.4" /note="NMA1701, lysC, aspartate kinase, len: 405aa; similar to many eg. SW:P26512 (AKAB_CORGL) lysC, aspartate kinase from Corynebacterium glutamicum (Brevibacterium flavum) (421 aa) fasta scores; E0: 0, 49.6% identity in 409 aa overlap. Contains Pfam match to entry PF00696 aakinese, Aspartate kinases, Glutamate kinases and Gamma glutamate phospho-reductases and Prosite match to PS00324 Aspartokinase signature." /codon_start=1 /transl_table=11 /product="aspartate kinase" /protein_id="CAB84929.1" /db_xref="GI:7380342" /db_xref="GOA:Q9JTN3" /db_xref="InterPro:IPR001048" /db_xref="InterPro:IPR001057" /db_xref="InterPro:IPR001341" /db_xref="InterPro:IPR002912" /db_xref="InterPro:IPR005260" /db_xref="UniProt/TrEMBL:Q9JTN3" /translation="MALIVHKYGGTSVGSPERIKNVAKRVAKARAEGHDIVVVVSAMS GETNRLVALAHMQEHPDPRELDVVLSTGEQVTIGLLAMALKDIGVDAKSYTGWQVAL KTDTAHTKARIESIDDEKMRADLTAGKVVTIVAGFQGISEGDISTLGRGSDTSAVAL AAALKADECQIYTDVDGVYTTDPRVVPPEARMDTVTFEEMIELASLGSKVLQIRSVF"

AGKYKVRRLRVLSSLQDGGNGTLITFEEDDNMERA AVT GIAFDKNQARINVRGVDPKPG
 VAYQILGAVADANIEVDMIIQNVGSEGTTFDSFTVPRGDYKQTL EILSERQDSIGAAS
 IDGDDTVCKVSAVGLGMRSHVGA AKIFRTLAEEGINIQMISTSEIKVSVLIDEKYME
 LATRVLHKAFNLG"

misc_feature 13..39
 /gene="lysC"
 /note="PS00324 Aspartokinase signature."
 misc_feature 205..882
 /gene="lysC"
 /note="Pfam match to entry PF00696 aakinase, Aspartate
 kinases, Glutamate kinases and Gamma glutamate
 phospho-reductases, score 114.30, E-value 2.3e-30"

ORIGIN

1 atggcgtaa tcgtacaaa atacggcggc acatccgtag gctgcccga acgcattaa
 61 aacgtggcca aacgtgtgc caaagcccgc gccgaaggac acgacatcgt cgtcgtcgt
 121 tccgccatga gcggtgaaac caaccgcctg gtcgcgttg gcacgaaat gcaggagcat
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 241 ttggcgatgg cattgaaaga catcgccgtg gatccaaaa gctacacagg ctggcaggtc
 301 gccacaaa ccgataccgc ccacacaaa gcccgatcg aaagcattga tgacgaaaaa
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 661 aagtacaaag tgcgcctgcg cgtactgagc agcctgcaag acggcgga tggcacctta
 721 attacctttg aagaggacga caacatggaa agagctgccg taaccggtat cgcattcgat
 781 aaaaaccaag cccgcacaa cgtgcgcggc gtacccgaca aaccgggtgt cgcctatcag
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 1021 gtgtcaaa tctccgcagt cggtttgggt atgcgttcgc acgtcggtgt agccgcaaa
 1081 atcttcgca cgctcgcca agagggtatc aacatccaaa tgattccac ctccgaaatc
 1141 aaagtctcg tattgattga tgaaaaatc atggaactgg caaccagggt attgcataaa
 1201 gcccttaatt tgggctga

//

[GENETYX : Amino Acid Sequence Homology Data]

Date : 2005.06.09

1st Amino Acid Sequence

File Name : Neisseria meningitidis_ask.prj
Sequence Size : 405

2nd Amino Acid Sequence

File Name : MM.prj
Sequence Size : 409

Unit Size to Compare = 2

Pick up Location = 1

[70.197% / 406 aa] INT/OPT.Score : < 870/ 1400 >

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1' MALIVHKYGG TSVGSPERIK NVAKRVAKAR AEGHDIVVVV SAMSGETNRL VALAHMQEH PDPRELDVVL
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1" MALIVQKYGG TSVANPERIR NVARRVARYK ALGHQVVVVV SAMSGETNRL ISLAKEIMQD PDPRELDVMV

71' STGEQVTIGL LAMALKDIGV DAKSYTGWQV ALKTDTAHTK ARIESIDDEK MRADLTAGKV VIVAGFQGIS
*****. *.**...*. ***** ** . **.* ** *** .**... ..**.* * *****..
71" STGEQVTIGM TALALMELGI KAKSYTGTQV KILTDDAFTK ARILDIDEHN LKKDLDDGYV CVVAGFQGVV

141' SEGDISTLGR GGSDTSAVAL AAALKADECQ IYTDVGVVYT TDPRVVPEAR RMDTVTFEEM IELASLGSKV
..*.*.**** *****..*** ***** ***** ***** **..****. ***** ****
141" ANGNITTLGR GGSDDTGVAL AAALKADECQ IYTDVGVVYT TDPRVVPEAR RLDKITFEEM LELASQGSKV

211' LQIRSVFAG KYKVLRLVLS SLQDGGNGTL ITFEE-DDNM ERAAVTGIAF DKNQARINVR GVPDKPGVAY
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211" LQIRSVFAG KYKVLRLVLS SFEEEGDGTI ITFEENEENM EEPIISGIAF NRDEAKITVT GVPDKPGIAY

280' QILGAVADAN IEVDMIIQNV GSEGTDFSF TVPRGDYKQT LEILSER-QD SIGAASIDGD DTVCKVSAVG
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281" QILGPVADAN IDVDMIIQNV GADGTTDFTF TVHKNEMNKA LSILRDKVQG HIQAREISGD DKIAKVSVVG

349' LGMRSHVGVA AKIFRTLAE GINIQMISTS EIKVSVLIDE KYMELATRVL HKAFNLG
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351" VGMRSHVGIA SQMFRTLAE GINIQMISTS EIKIAVVIEE KYMELAVRVL HKAFGLENA

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DDPS

1: AF065159. Reports Bradyrhizobium ja...[gi:6655022] Links

LOCUS AF065159 891 bp DNA linear BCT 03-JAN-2000

DEFINITION Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydrodipicolinate synthase (dapA), MscL (mscL), SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/SpoT homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele, complete cds; RNase III (rnc), GTP-binding protein Era (era), hypothetical protein, recO-like protein, topoisomerase II (gyrA), putative ABC transporter, putative GMC-oxidoreductase, hypothetical protein, putative cytochrome C binding protein (cyc4), putative polytopic integral membrane protein, superoxide dismutase SodM-like protein, putative inner membrane protein, AttM-like protein (attM), adenylate cyclases-like protein, and putative inner membrane protein (spcT) genes, complete cds; and unknown genes.

ACCESSION AF065159 REGION: 4811..5701

VERSION AF065159.3 GI:6655022

KEYWORDS

SOURCE Bradyrhizobium japonicum

ORGANISM Bradyrhizobium japonicum

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Bradyrhizobiaceae; Bradyrhizobium.

REFERENCE 1 (bases 1 to 891)

AUTHORS Mueller,P. and Stingel,D.

TITLE Extended DNA sequencing in the upstream region of sipF in
Bradyrhizobium japonicum

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 891)

AUTHORS Mueller,P. and Stingel,D.

TITLE Direct Submission

JOURNAL Submitted (27-OCT-1999) Biology, Philipps Universitaet Marburg.

Karl-von-Frisch-Strasse, Marburg 35032, Germany

REMARK Sequence update by submitter

REFERENCE 3 (bases 1 to 891)

AUTHORS Mueller,P. and Stingel,D.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-2000) Biology, Philipps Universitaet Marburg,

Karl-von-Frisch-Strasse, Marburg 35032, Germany

REMARK Sequence update by submitter

COMMENT On Jan 3, 2000 this sequence version replaced gi:6136295.

FEATURES Location/Qualifiers

source 1..891

/organism="Bradyrhizobium japonicum"

/mol_type="genomic DNA"

/strain="USDA 110spc4"

/db_xref="taxon:375"

gene 1..891

/gene="dapA"

CDS 1..891

/gene="dapA"

/function="involved in the biosynthesis of the rhizopine

3-O-methyl-scylo-inosamine"

/function="catalyzes the first step in the biosynthesis of
diaminopimelate and lysine from aspartate semialdehyde"

/note="similar to the MosA protein of Sinorhizobium
meliloti; belongs to the DHDPS family"

/codon_start=1

/transl_table=11

/product="dihydrodipicolinate synthase"

/protein_id="AAF04320.1"

/db_xref="GI:6136299"

/translation="MAAKTKFRGSFTALVTPFKNGSLDEAAFRSLVNWQISEGTNGLV

PVGTTGESPTLSHDEHKKVVEWCIEEAKGRVPVAGAGSNSTKEAIELAQHA EKAGAD

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IAGVKDATASMRVRSQQRAAMGEDFNQLSGEVATILGYMAQCGHGCISVTSNVAPRLC

SEFHTAWQKGDQRTALKLHDKLMPVHNNLFIESNPAPIKYAMSLLGKLDLRLPMVP

VTEPTRVAVRSAMVHAGLIN"

ORIGIN

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61 ggctcgctcg acgaggcagc gttccgctcc ctggtcaact ggcagatttc cgagggcacc
121 aacggactgg tcccggtcgg cagcacaggc gagagccga cgtcagcca tgacgagcac
181 aagaaggtcg tcgagtggcg catcgaggag gccaagggcc gcgtgcccggt ggttgcgggt
241 gccggctcca actcgaccaa ggaggcgatc gagtggccc agcacgccga gaaggcgggc
301 gccgacgccg tgctgggtgt gacgccttac tacaacaagc cgaccagga agggatgtac
361 cagcattca aggcgatcaa cgtatcgatc gggattcaa tcatattta caacatccc
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481 atcccgccg tcaaggacgc caccgccagc atggtccgcg tctcgagca gcgtgccg
541 atggcgagg acttcaacca gctctgggc gaggtagcga ccactctgg ctacatggcc
601 caatcgccc accgctgcat ctgggtgacc tgaacgtcg caccgcgct gtgctggag
661 ttccacacc cctggcagaa gggcgatcaa cgcaccgcgc tgaagctga cgacaagctg
721 atcccgctgc acaacaacct cttcatcgag agcaatccgg cgcgatcaa gtacgcatg
781 tcgctgctcg gcaagcttga cgagacgtg cggctgccga tgggtccggt gaccgagcca
841 acgcgcgttg cgtgcgag cgccatggtt cagctggcc tgatcaactg a

//

DDPS-2

NC_003116. Reports *Neisseria meningi...*[gi:15793034] Links

LOCUS NC_003116 876 bp DNA linear BCT 19-MAY-2005

DEFINITION *Neisseria meningitidis* Z2491, complete genome.

ACCESSION NC_003116 REGION: complement(1073966..1074841)

VERSION NC_003116.1 GI:15793034

KEYWORDS

SOURCE *Neisseria meningitidis* Z2491

ORGANISM *Neisseria meningitidis* Z2491

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; *Neisseria*.

REFERENCE 1 (bases 1 to 876)

AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,

Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,

Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,

Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,

Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,

Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.

TITLE Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491

JOURNAL Nature 404 (6777), 502-506 (2000)

PUBMED 10761919

REFERENCE 2 (bases 1 to 876)

AUTHORS

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (27-SEP-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 876)

AUTHORS Parkhill,J.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2000) Sanger Centre. Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, United Kingdom

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AL157959.

COMPLETENESS: full length.

FEATURES	Location/Qualifiers
source	1..876 /organism="Neisseria meningitidis Z2491" /mol_type="genomic DNA" /db_xref="taxon:122587" /serogroup="A"
gene	1..876 /gene="dapA" /locus_tag="NMA1124" /db_xref="GeneID:907093"
CDS	1..876 /gene="dapA" /locus_tag="NMA1124" /EC_number="4.2.1.52" /codon_start=1 /transl_table=11 <u>/product="dihydrodipicolinate synthase"</u> /protein_id="NP_283893.1" /db_xref="GI:15794071" /db_xref="CDD:pfam00701" /db_xref="COG:COG0329" /db_xref="GeneID:907093" /translation="MLQGSLVALITPMNQDGSIHYEQLRDLIDWHIENGTDGIVAVGT TGESATLSVEEHTAVIEAVVKHVAKRVPVIAGTGANNNTVEAIALSQAAEKAGADYTLS VVPYYNKPSQEGMYRHFKAFAEAAAIPMILYNVPGRTVVSMNNETILRLAEIPNIVGV KEASGNIGSNIELINRAPEGFVVLSGDDHTALPFMLCGGHGVITVAANAAPKLFADMC RAALQGDIALARELNDRLIPIYDTMFCEPSAAPKWAVSALGRCEPHVRLPLVPLTEG GQAKVRAALKASGQL"

ORIGIN

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1 atgttacaag gtagcctggt tgccctgatt accccgatga atcaagacgg cagcatccat
61 tacgaacaac tccgcgactt aatcgactgg cacattgaaa acggcacgga cgcatcgtc
121 gccgtcgcca cgacaggcga atccgccacc ctctccgtcg aagaacacac cgccgtcatc
181 gaagccgtcg tcaaacacgt tgccaaacgc gtccccgtca tcgccggcac aggggcaaac
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11

Date : 2005.06.09

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File Name      : Neisseria meningitidis_DDPS.prj
Sequence Size  : 291
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File Name      : MM+4.prj
Sequence Size  : 296
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Unit Size to Compare = 2
Pick up Location      = 1
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```

1'      MLOGSL VALITPMNQD GSIHYEQLRD LIDWHIENG T DGIVAVGTTG ESATLSVEEH TAVIEAVVKH
      ** *** **.*.*.*.* *...*.*** **.*.*.* **.*.*.*
1"      MALGMLTGSL VAIVTPMFED GRDLDLALKK LVDFHVEAGT DGIVIVGTTG ESPTVDVDEH CLLIKTTIEH

67'     VAKRVPVIAG TGANNTVEAI ALSQAAEKAG ADYTLSVVPY YNKPSQEGMY RHFKAVAEAA AIPMILYNVP
      ***** **.*.*.* **.*.*.* **.*.*.* *****.* *****.* *****
71"     VAKRVPVIAG TGANSTAEAI ELTAKAKALG ADACLLVAPY YNKPSQEGLY QHFKAVAEAV DIPQILYNVP

137'    GRTVVMNNE TILRLAEIPN IVGKEASGN IGSNIELINR APEGFVVLGS DDHTALPFML CGGHGVITVA
      *** **.*.*.* **.*.*.* *...*.*** **.*.*.* **.*.*.* **.*.*.*
141"    GRTGCDLSND TVLRLAQIRN IVGIKDATGG IERGTDLLLR APADFAIYSG DDATAALALML LGGKGVISVT

207'    ANAAPKLFAD MCRAALQGDI ALARELNDR L IPIYDTMFCE PSPAAPKWAV SALGRCEPHV RLPLVPLTEG
      **.*.*.* **.*.*.* **.*.*.* .....* **.*.*.* **.*.*.*
211"    ANVAPKLMHE MCEHALNGNL AAACAANAKL FALHQKLFVE ANPIPVKWL QQMGMATGI RLPLVNLSSQ

277'    GQAKVRAALK ASGQL
      ..*.*.*
281"    YHEVLRNAMK QAEIAA

```


1'	MALGMLTGSL	VAIVTPMFED	GRLLDLALKK	LVDFHVEAGT	DGIVIVGTTG	ESPTVDVDEH	CLLIKTTTIEH
	*.***.	***** *	*. *	*.***.***	..** *****	***... ***	... **.
1"	MFTGSI	VAIVTPMDEK	GNVCRASLKK	LIDYHVASGT	SAIVSVGTTG	ESATLNHDEH	ADVMMTLDL
71'	VAKRVPVIAG	TGANSTAEAI	ELTAKAKALG	ADACLIVAPY	YNKPSQEGLY	QHFKAVAEAV	DIPQILYNVP
	..*.*****	****.*****	***... *	..** *.***	**..*****	*****..*	*.*****.
67"	ADGRIPVIAG	TGANATAEAI	SLTQRFNDSG	IVGCLTVTPY	YNRPSQEGLY	QHFKAIAEHT	DLPQILYNVP
141'	GRTGCDLSND	TVLRLAQIRN	IVGIKDATGG	IERTDILLR	APADFAIYSG	DDATALALML	LGGKGVISVT
	*****.	** *****	*.*****.	..**** **	*****..*	*****.
137"	SRTGCDLPE	TVGRLAKVKN	IIGIKEATGN	LTRVNQIKEL	VSDDFVLLSG	DDASALDFMQ	LGGHGVISVT
211'	ANVAPKLMHE	MCEHALNGNL	AAAKAANAKL	FALHQKLFVE	ANPIPVKMWL	QOMGMIATG-	IRLPLVNLSS
	.. *	** * ...	*.* *.. *	..** **	*****.	...***.	***... .
207"	ANVAARDMAQ	MCKLAAEGHF	AEARVINQRL	MPLHNKLFVE	PNPIPVKWAC	KELGLVATDT	LRLPMTPTID
280'	QYHEVLNRNAM	KQAEIAA					
	***..*	*.*..					
277"	SGRETVRAAL	KHAGLL					

[GENETYX : Amino Acid Sequence Homology Data]

Date : 2005.05.30

1st Amino Acid Sequence

File Name : M.methylotrophus-lysCaa.prj
Sequence Size : 409

2nd Amino Acid Sequence

File Name : Escherichia coli-lysC.prj
Sequence Size : 449

[26.849% / 365 aa] INT/OPT.Score : < 119/ 321 >

1'		MALIV QKYGGTSVAN PERIRNVARR
1"	MSEIVVSKFG GTSVADFDM NRSADIVLSD ANVRLVVLVA SAGITNLLVA LAEGLEPGER FEKLDAIRNI	
26'	VARYKALGHQ VVVVVSAMSG ETNRLISLAK EIMQDDPRE LDVMVSTGEQ VTIGMTALAL MELGIKAKSY	
71"	QFAILERLRY PNVIREEIER LLENITVIAE AAALATSPAL TDELVSHGEL MSTLLFVEIL RERDVQAQWF	
96'	TGTQVKILTD DAFTK----- ARILDIDEHN LKKDLDDGYV CVVAGFQGV D ANGNITTLGR GGSDDTTGVAL	
141"	DVRKV-MRTN DRFGRAEPDI AALAEALALQ LLPRINEGLV -ITQGFICSE NKGRTTTTLGR GGSDDYTAALL	
161'	AAALKADECQ IYTDVDGVYT TDP RVVPEAR RLDKITFEEM LELASQSKV LQIRSVFEFAG KYKVKLRVLS	
209"	AEALHASRVD IWTDVPGIYT TDP RVVSAK RIDEIAFAEA AEMATFGAKV LHPATLLPAV RSDIPVFVGS	
231'	SFEEEGDGL ITFEENEENM EEP IISGIAF NRDEAKITVT GVP--DKPGI AYQILGPVAD ANIDVDMIIQ	
279"	SKDPRAGGTL VC-----NKTE NPPLFRALAL RRNQTLLTLH SLNMLHSRGF LAEVFGILAR HNISVDLIT-	
299'	NVGADGTTDF TFTVHKNE MN KALSILRDKV QGHIQAR-EI SGDDKIAKVS VVGVMGRSHV GIASQMFTL	
344"	--TSEVSVAL TLDT-TGSTS TGD TLLTQSL LMELSALCRV EVEEGLALVA LIGNDLSKAC GVGKEVFGVL	
368'	AEEGINIQMI STSEIKIAVV IEKYMELAV RVLHKAFGLE NA	
411"	EPFNIRMICY GASSHNLCFL VPGEDAEQVV QKLHSLNLF	